

B¹ CONT represents Val or Ile, in that they belong to the urotensin II family and in that they exhibit at least 45%, and preferably at least 70%, similarity with the polypeptide sequence SEQ ID NO:1, corresponding to human preprourotensin II.

Please replace the paragraph at page 10, prenumbered line 32 to page 11, prenumbered line 2, as follows:

- Figure 1 illustrates the alignment of the deduced amino acid sequences of, respectively, human, frog (SEQ ID NO. 46) and carp prepro-UII (SEQ ID NOS. 47 and 48).

B² In this figure, the signal sequence is indicated in italics; the conserved amino acids are indicated in black; the cleavage sites of the prohormone are indicated by stars and the conserved amino acid residues are indicated by a black circle. The disulfide bridge present in the UII sequence is indicated under the urotensin II sequence. The amino acids are numbered on the right of the figure;

Please replace the paragraph at page 11, prenumbered lines 32-37, as follows:

B³ - Figure 6 is a comparison of the primary structures of urotensin II from various species (SEQ ID NOS. 49-64). Dashes have been inserted in order for the sequences to be optimally aligned. The dots illustrate the amino acids residues which are identical between the various sequences, with respect to the human sequence;

Page 21 (Abstract), after the last line, beginning on the next page, please delete the Sequence Listing at pages 1-18 and insert the substitute Sequence Listing attached hereto.